### Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

### Listing of Claims:

1. (Previously presented)  A method for designing a specific polyamide

$$X_1X_2\ldots X_m\text{-}\gamma\text{-}X_{(m+1)}\ldots X_{(2m-1)}X_{2m}\text{-}R_1$$

wherein

$X_1$, $X_2$, $X_m$, $X_{(m+1)}$, $X_{(2m-1)}$, and $X_{2m}$ are carboxamide residues forming carboxamide

binding pairs $X_1/X_{2m}$, $X_2/X_{(2m-1)}$, $X_m/X_{(m+1)}$;

$\gamma$ is $\gamma$-aminobutyric acid or 2,4 diaminobutyric acid, and

$R_1$ is $-NH(CH_2)_{0\text{-}100}NR_2R_3$, $-NH(CH_2)_{0\text{-}12}CONH(CH_2)_{0\text{-}100}NR_2R_3$, or $-NHR_2$, where $R_2$

and $R_3$ are independently selected from the group consisting of H, Cl, NO, N-acetyl, benzyl, $C_{1\text{-}}$

$_{100}$ alkyl, $C_{1\text{-}100}$ alkylamine, $C_{1\text{-}100}$ alkyldiamine, $C_{1\text{-}100}$ alkylcarboxylate, $C_{1\text{-}100}$ alkenyl, a $C_{1\text{-}100}$

alkynyl, and $C_{1\text{-}100}$ alkyl-L, where L is selected from the group consisting of arylboronic acids,

biotins, polyhistidines comprised from about 2 to 8 amino acids, haptens, solid phase supports,

oligodeoxynucleotides, N-ethylnitrosourea, fluorescein, bromoacetamide, iodoacetamide, DL-α-

lipoic acid, acridine, captothesin, pyrene, mitomycin, texas red, anthracene, anthrinilic acid,

avidin, DAPI, and oligodeoxynucleotide, isosulfan blue, malachite green, psoralen, ethyl red, 4-

(psoraen-8-yloxy)-butyrate, tartaric acid, and (+)-α-tocopheral, suitable for use as a DNA-binding

ligand that is selective for identified target DNA-sequences 5'-$WN_1N_2\ldots N_mW$-3' where m is

an integer having a value from 3 to 6, the method comprising:

-2-

DLMR254455.1

PAGE 5/13 * RCVD AT 6/10/2004 12:40:30 PM [Eastern Daylight Time] * SVR:USPTO-EFXRF-1/0 * DNIS:8729306 * CSID: * DURATION (mm-ss):03-04

(a)     identifying a target sequence of double stranded DNA having the form 5'-WN$_1$N$_2$ ... N$_m$W-3', N$_1$N$_2$ ... N$_m$ being the sequence to be bound by carboxamide residues, wherein each N is independently chosen from the group A, G, C, and T, each W is independently chosen from the group A and T, and m is an integer having a value from 3 to 6;

(b)     representing the identified sequence as 5'-W*ab* ... *x*W-3', wherein *a* is a first nucleotide to be bound by the X$_1$ carboxamide residue, *b* is a second nucleotide to be bound by the X$_2$ carboxamide residue, and *x* is the corresponding nucleotide to be bound by the X$_m$ carboxamide residue;

(c)     defining *a* as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified sequence;

(d)     selecting Im as the X$_1$ carboxamide residue and Py as the X$_{2m}$ carboxamide residue if a = G;

(e)     selecting Py as the X$_1$ carboxamide residue and Im as the X$_{2m}$ carboxamide residue if *a* = C;

(f)     selecting Hp as the X$_1$ carboxamide residue and Py as the X$_{2m}$ carboxamide residue if *a* = T;

(g)     selecting Py as the X$_1$ carboxamide residue and Hp as the X$_{2m}$ carboxamide residue if *a* = A; and

(h)     repeating steps c – g for *b* through *x* until all carboxamide residues are selected;

-3-

wherein Im is N-methylimidazole, Hp is 3-hydroxy-N-methylpyrrole , Py is N-methylpyrrole, A is adenine, G is guanine, C is cytosine, and T is thymine; and

synthesizing the polyamide.

2. (Cancelled)

3. (Previously presented)  The method of claim 1 further comprising the step of determining if the binding affinity of the polyamide to the identified target sequence is subnanomolar.

4. (Previously presented)  The method of claim 1 further comprising the step of determining if the polyamide exhibits a binding affinity that is at least ten-fold higher for said identified target sequence compared to a non-target DNA sequence.

5. (Previously presented)  The method of claim 1 further comprising the step of replacing at least one pyrrole residue with a β-alanine residue.

6-41. (Cancelled)

42. (Previously presented)  The method of claim 1 wherein the identified target DNA sequence is a regulatory sequence.

43. (Previously presented)  The method of claim 1 wherein the identified target DNA sequence is a promoter sequence.

44. (Previously presented)  The method of claim 1 wherein the identified target DNA sequence is a coding sequence.

-4-

45. (Previously presented) The method of claim 1 wherein the identified target DNA sequence is a non-coding sequence.

46. (Previously presented) A polyamide composition produced by the method of claim 1 wherein the binding of the carboxamide binding pairs to the identified target DNA sequence modulates the expression of a gene.

47. (Previously presented) A composition comprising an effective amount of a polyamide produced by the method of claim 1 and a pharmacologically suitable excipient.

48. (Previously presented) A diagnostic kit comprising a polyamide produced by the method of claim 1.

49. (Previously presented) A polyamide designed by the method of claim 1, having the structure:
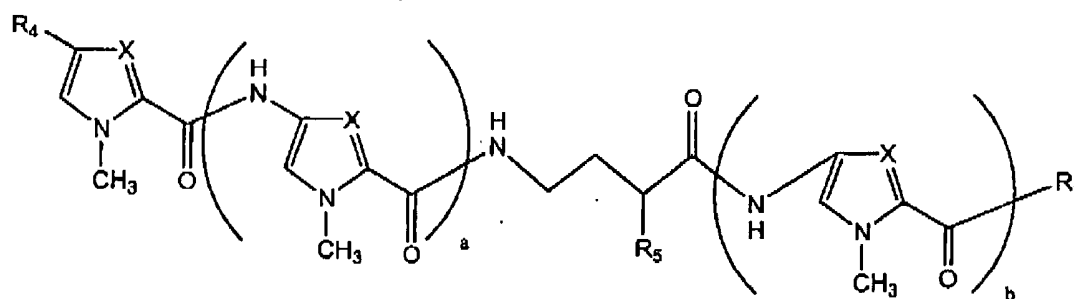


wherein

$R_4$ is selected from the group consisting of H, $NH_2$, SH, Cl, Br, F, N-acetyl, and N-formyl;

$R_5$ is H or $NH_2$;

-5-

DLMR254455.1

PAGE 8/13 * RCVD AT 6/10/2004 12:40:30 PM [Eastern Daylight Time] * SVR:USPTO-EFXRF-1/0 * DNIS:8729306 * CSID: * DURATION (mm-ss):03-04

$R_1$ is $-NH(CH_2)_{0-100}NR_2R_3$, $-NH(CH_2)_{0-12}CONH(CH_2)_{0-100}NR_2R_3$, or $-NHR_2$, where $R_2$ and $R_3$ are independently selected from the group consisting of H, Cl, NO, N-acetyl, benzyl, $C_{1-100}$ alkyl, $C_{1-100}$ alkylamine, $C_{1-100}$ alkyldiamine, $C_{1-100}$ alkylcarboxylate, $C_{1-100}$ alkenyl, a $C_{1-100}$ alkynyl, and $C_{1-100}$ alkyl-L, where L is selected from the group consisting of arylboronic acids, biotins, polyhistidines comprised from about 2 to 8 amino acids, haptens, solid phase supports, oligodeoxynucleotides, N-ethylnitrosourea, fluorescein, bromoacetamide, iodoacetamide, DL-α-lipoic acid, acridine, captothesin, pyrene, mitomycin, texas red, anthracene, anthrinilic acid, avidin, DAPI, and oligodeoxynucleotide, isosulfan blue, malachite green, psoralen, ethyl red, 4-(psoraen-8-yloxy)-butyrate, tartaric acid, and (+)-α-tocopheral;

each X is independently selected from the group consisting of N, CH, and COH;

each a is an integer from 2 to 5; and

each b is an integer from 3 to 6.

50. (New)   A method for designing a specific polyamide

$$X_1X_2 \ldots X_m\text{-}\gamma\text{-}X_{(m+1)} \ldots X_{(2m-1)}X_{2m}\text{-}R_1$$

wherein

$X_1$, $X_2$, $X_m$, $X_{(m+1)}$, $X_{(2m-1)}$, and $X_{2m}$ are carboxamide residues forming carboxamide binding pairs $X_1/X_{2m}$, $X_2/X_{(2m-1)}$, $X_m/X_{(m+1)}$, and wherein one carboxamide binding pair is substituted with a $\beta/\beta$, wherein $\beta$ is β-alanine;

γ is γ-aminobutyric acid or 2,4 diaminobutyric acid, and

-6-

$R_1$ is $-NH(CH_2)_{0-100}NR_2R_3$, $-NH(CH_2)_{0-12}CONH(CH_2)_{0-100}NR_2R_3$, or $-NHR_2$, where $R_2$ and $R_3$ are independently selected from the group consisting of H, Cl, NO, N-acetyl, benzyl, $C_{1-100}$ alkyl, $C_{1-100}$ alkylamine, $C_{1-100}$ alkyldiamine, $C_{1-100}$ alkylcarboxylate, $C_{1-100}$ alkenyl, a $C_{1-100}$ alkynyl, and $C_{1-100}$ alkyl-L, where L is selected from the group consisting of arylboronic acids, biotins, polyhistidines comprised from about 2 to 8 amino acids, haptens, solid phase supports, oligodeoxynucleotides, N-ethylnitrosourea, fluorescein, bromoacetamide, iodoacetamide, DL-α-lipoic acid, acridine, captothesin, pyrene, mitomycin, texas red, anthracene, anthrinilic acid, avidin, DAPI, and oligodeoxynucleotide, isosulfan blue, malachite green, psoralen, ethyl red, 4-(psoraen-8-yloxy)-butyrate, tartaric acid, and (+)-α-tocopheral, suitable for use as a DNA-binding ligand that is selective for identified target DNA-sequences 5'-WN$_1$N$_2$ ... N$_m$W-3' where m is an integer having a value from 3 to 6, the method comprising:

(a)     identifying a target sequence of double stranded DNA having the form 5'-WN$_1$N$_2$ ... N$_m$W-3', N$_1$N$_2$ ... N$_m$ being the sequence to be bound by carboxamide residues, wherein each N is independently chosen from the group A, G, C, and T, each W is independently chosen from the group A and T, and m is an integer having a value from 3 to 6;

(b)     representing the identified sequence as 5'-W$ab$ ... $x$W-3', wherein $a$ is a first nucleotide to be bound by the X$_1$ carboxamide residue, $b$ is a second nucleotide to be bound by the X$_2$ carboxamide residue, and $x$ is the corresponding nucleotide to be bound by the X$_m$ carboxamide residue;

(c)     defining $a$ as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified sequence;

-7-

(d)      selecting Im as the $X_1$ carboxamide residue and Py as the $X_{2m}$ carboxamide residue if a = G;

(e)      selecting Py as the $X_1$ carboxamide residue and Im as the $X_{2m}$ carboxamide residue if $a$ = C;

(f)      selecting Hp as the $X_1$ carboxamide residue and Py as the $X_{2m}$ carboxamide residue if $a$ = T;

(g)      selecting Py as the $X_1$ carboxamide residue and Hp as the $X_{2m}$ carboxamide residue if $a$ = A; and

(h)      repeating steps c – g for $b$ through $x$ until all carboxamide residues are selected;

wherein Im is N-methylimidazole, Hp is 3-hydroxy-N-methylpyrrole , Py is N-methylpyrrole, A is adenine, G is guanine, C is cytosine, and T is thymine; and

synthesizing the polyamide.